| 1 | GAATICGCACGAGGTTTTTTTTTTTTTTTTTTTCCCCTCTTTTCTTTC | 60 |
|-----|--|-----|
| 61 | ATCCGAAAGAGCTGTCAGCCGCCGGGCTGCACCTAAAGGCGTCGGTAGGGGGATAAC | 120 |
| 121 | AGTCAGAGACCCTCCTGAAAGCAGGAGACGGGACGCTACCCCTCCGGCTCTGCGGGGCGG | 180 |
| 181 | CTGCGGCCCTCCGTTCTTTCCCCCTCCCCAGAGACACTCTTCCTTTCCCCCACGAAG | 240 |
| 241 | ACACAGGGGCAGGAACGCGAGGGCTGCCCCTCCGCCATGGGAGGCCGCTTCCTGCTGACG | 300 |



| | CTCGCCCTCCTCGCGCGCTGCTGTGCCGGGTTGACGGCTCCGGGGTTCGAG | 60 |
|-----|--|------|
| 301 | | ,,,, |
| | | |
| | • | |
| | | |
| | CTGAAGCTGCAGGAGTTTGTCAACAAGAAGGGGCTGCTCAGCAACCGCAACTGCTGCCGG | 120 |
| 361 | | |
| | | |
| | | |
| | | |
| | | |
| 421 | GGGGGGGCCCGGAGGCGCCGGCAGCAGCAGTGCGACTGCAAGACCTTCTTCCGCGTC | 180 |
| | | |
| | | |
| | | |
| | | |
| | TGCCTGAAGCACTACCAGGCCAGCGTCTCCCCCGAGCCGCCCTGCACCTACGGCAGCGCC | 540 |
| 481 | | |
| | | |
| | | |
| | | |
| 541 | ATCACCCCGTCCTCGGCGCCAACTCCTTCA3CGTCCCCGACGGCGGGGGGGGCGCCGAC | 600 |
| | | |
| | | |
| | | |
| | | |
| | CCCGCCTTCAGCAACCCCATCCGCTTCCCCTTCGGCTTCACCTGGCCCGGCACCTTCTCG | 660 |
| 601 | | 000 |
| | • | |
| | • | |
| | CTCATCATCGAGGCTCTGCACACCGACTCCCCGACGACCTCACCACAGAAAACCCCGAG | |
| 661 | CICATCATCOROCATCACACACACACACACACACACACACACACACACACA | 720 |

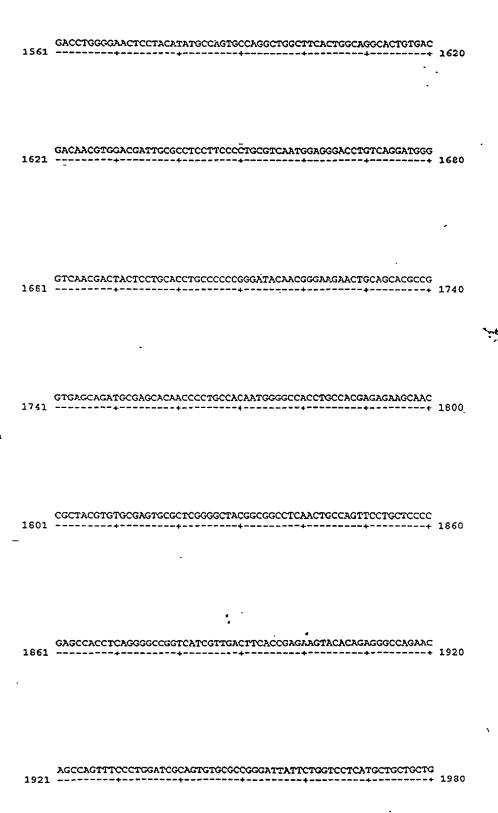
| | COCCTCATCAGCCCCCAGCCACCCAGAGCACCTGGCGGTGGGGGTGGAGGAGTGGTCCCAG | |
|------|---|------|
| 721 | | 780 |
| | | |
| 781 | GACCTGCACAGCAGCGGCCGGACCGACCTCAAGTACTCCTATCGCTTTGTGTGTG | 840 |
| | _ • | - |
| 841 | CACTACTACGGGGAAGGCTGCTCTGTCTTCTGCCGGCCCCGTGACGACCGCTTCGGTCAC | 900 |
| | · | - |
| 901 | TTCACCTGTGGAGAGCGTGGAGAGGGCCAGTACTGC | 960 |
| | ACTGAGCCGATTTGCTTGCCTGGGTGTGACGAGCAGCAGCACGCCTTCTGCGACAAACCTGGG | • |
| 961 | | - |
| 1021 | GAATGCRAGTGCAGAGTGGUTTGGCAGGGGCGGTACTGTGACGAGTGCATCCGATACCCA | 1080 |
| | • | |
| 1081 | GGCTGCCTGCACGGTACCTGTCAGCAGCCATGGCAGTGCAACTGCCAGGAAGGCTGGGGG | 1140 |

FIG. 1A (cont'd)



| 1141 | GGCCTTTTCTGCAACCAGGACCTGAACTACTGCACTCACCACAAGCCATGCAAGAATGGT | 1200 |
|------|--|------|
| 1201 | CGGTGTACGTGGTTGTGGCCAGTCCCCTCGATGTGAACAAGAACGGCTGGACCCATGTGT | 3260 |
| 1261 | GGCTCCAGCTGCGAGATTGAAAYCAACGAATGTGATGCCAACCCTTGCAAGAATGGTGGA | |
| | AGCTGCACGGATCTCGAGAACAGCTATTCCTGTACCTGCCCCCCAGGCTTCTATGGTAAA | |
| 1321 | | 1380 |
| 1381 | AACTGTGAGCTGAGTGCAATGACTTGTGCTGATGGACCGTGCTTCAATGGAGGGCGATGC | 1440 |
| 1441 | ACTGACAACCCTGATGGGGTACAGCTGCCGCTGCCCACTGGGTTATTCTGGGTTCAAC | 1500 |
| 1501 | TGTGAAAAGAAAATCGATTACTGCAGTTCCAGCCCTTGTGCTAATGGAGCCCAGTGCGTT | 1560 |

FIG. 1A (cont'd)



TACCAGTCGGTGTACGTCATATCAGAAGAGAAAGATGAGTGCATCATAGCAACTGAGGTG

TAAAACAGACGTGACGTGGCAAAGCTTATCGATACCGTCATCAAGCTT
2461 ------ 2508

. : 5

| 1 | GAATTCCGCACGAGGTTTTTTTTTTTTTTTTTCCCCTCTTTTCTTTTCTTTTCCTTTT | 69 |
|------------------|---|-----|
| 70 | AGCTGTCAGCCGCCGCGCGCTCCACCTAAAGGCGTCGGTAGGGGGATAACAGTCAGAGACCCTCCTGA | 138 |
| 139 | - AAGCAGGAGACGGTACCCCTCCGGCTCTGCGGGGCGCCCCTCCGTTCTTTCCCCCTC | 207 |
| 208 | CCCGAGAGACACTCTTCCTTTCCCCCCACGAAGACACA:SGGGCAGGAACGCGAGGGGCGCTGCCCCTCCGCC | 276 |
| 277 _: | ATGGGAGGCCGCTTCCTGCTGACGCTCCCCCTCCTCCCGCGCTGCCAGGTTGACGGC | 345 |
| 346 | TCCGGGGTGTTCGAGCTGAAGCTGCAGGAGTTTGTCAACAAGAAGGGGGCTGCTCAGCAACCGCAACTGC : | 414 |
| 415 | . TGCCGGGGGGGGCCCCGGAGGCGCCAGCAGCAGCAGCAGCTGCAAGACCTTCTTCCGCGTCTGC | 483 |



484 CTGAAGCACTACCAGGCCAGCGTCTCCCCCGAGCCGCCCTGCACCTACGGCAGCGCCAT

622 CGCTTCCCCTTCGGCTTCACCTGGCCCGGCACCTTCTCGCTCATCATCGAGGCTCTGC

691 CCCGACGACCTCACCACAGAAAACCCCGAGCGCCTCATCAGCCGCCTGGCCACCCAGA

760 GTGGGCGAGGAGTGCTCCCAGGACCTGCACAGCAGCGCCGCACCGCACCTCAAGTAC

GTGTGATGAGCACTACTACGGGGAAGGCTGCTCTGTCTTCTGGGGGCCCCGTGACGACGCTTCGGT 897

898(CACTTCACCTGTGGAGAGGGTGGCGAGAAGGTCTGCAACCCAGGCTGGAAGGGCCAGTACTGCACTGAG 966

967 CCGATTTGCTTGCCTGGGTGTGACGAGCAGCACGCTTCTGCGACAAACCTGGGGAATGCAAGTGCAGA 1035

1105 CAGCCATGGCAGCTGCAACTGCCAGGAAGGCTGGGGCCCTTTTCTGCAACCAGGACCTGAACTACTGC 1173

1174 ACTCACCACAAGCCATGCAAGAATGGTGCCACATGCACCAACACCGGTCAGGGGGAGCTACACTTGTTCT 1242

1243 TGCCGACCTGGGTACACAGGCTCCAGCTGCGAGATTGAATCAACGAATGTGATGCCAACCCTTGCAAG 1311



1312 AATGGTGGAAGCTGCACGGATCTCGAGAACAGCTATTCCTGTACCTGCCCCCCAGGCTTCTATGGTAAA 1380

1381 AACTGTGAGCTGAGTGCAATGACTTGTGCTGATGGACCGTGCTTCAATGGAGGGCGATGCACTGACAAC 1449

1450 CCTGATGGTGGATACAGCTGCCGCTGCCCACTGGGTTATTCTGGGTTCAACTGTGAAAAGAAAATCGAT 1518

1519 TACTGCAGTTCCAGCCCTTGTGCTAATGGAGCCCAGTGCGTTGACCTGGGGAACTCCTACATATGCCAG 1587

1588 TGCCAGGCTGGCTTCACTGGCAGGCACTGTGACGACAACGTGGACGATTGCGCCTCCCTTCCCCTGCGTC 1656

1657 AATGGAGGGACCTGTCAGGATGGGGTCAACGACTACTCCTGCACCTGCCCCCCGGGATACAACGGGAAG 1725

1726 AACTGCAGCACGCCGGTGAGCAGATGCGACCACAACCCCTGCCACAATGGGGCCACCTGCCACGAGAGA 1794

1795 AGCAACCGCTACGTGTGCGAGTGCGCTCCGGGGCTACGGCGGCCTCAACTGCCAGTTCCTGCTCCCGAG 1863

1864 CCACCTCAGGGCCGGTCATCGTTGACTTCACCGAGAAGTACACAGAGGGCCAGAACAGCCAGTTTCCC 1932

1933 TGGATCGCAGTGTGCGCCGGGATTATTCTGGTCCTCATGCTGCTGCTGGGTTGCGCCGCCATCGTCGTC 2001

2002 TGCGTCAGGCTGAAGGTGCAGAAGAGGCCACCACCACCACCCCGAGTCCTGCAGGAGTGAAACGGAGACCATG 2070

2071 AACAACCTGGCGAACTGCCAGCGCGAGAAGGACATCTCCATCAGCGTCATCGGTGCCACTCAGATTAAA 2139

2140 AACACAAATAAGAAAGTAGĀCTTTCACAGCGATAACTCCGATAAAAACGGCTACAAAGTTAGATACCCA 2208



2209 TCAGTGGATTACAATTTGGTGCATGAACTCAAGAATGAGGACTCTGTGAAAGAGGAGCATGGCAAATGC 2277

2278 GAAGCCAAGTGTGAAACGTATGATTCAGAGGCAGAAGAGAAAAGCCACTACAGCTAAAAACTAGTGAC 2346

2347 ACTTCTGAAAGAAAACGGCCAGATTCAGTATATTCCACTTCAAAGGACACAAAGTACCAGTCGGTGTAC 2415

2416 GTCATATCAGAAGAGAAGATGAGTGCATCATAGCAACTGAGTTAGTATCCCACCTGGCAETCGGACA 2484

2485 AGTCT FGGTGTGTGATTCCCATC PAGCGCACGGCGGCCAAACCATTCTACCTGCTGCCACAGTC 2553

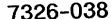
2554 ATCTGTACCCAATGAAAACTGGCCACCTTCAGTCTGTGGCACTGCAGACGTTGAAAAAACTTGTTGTGG 2622

2692 GTTGTAGCTTACTAACCCTACTGACTCATTCTTTCGTGTGCTTCCTGCAGAGCCTGTTTTTGCTTGGCA 2760

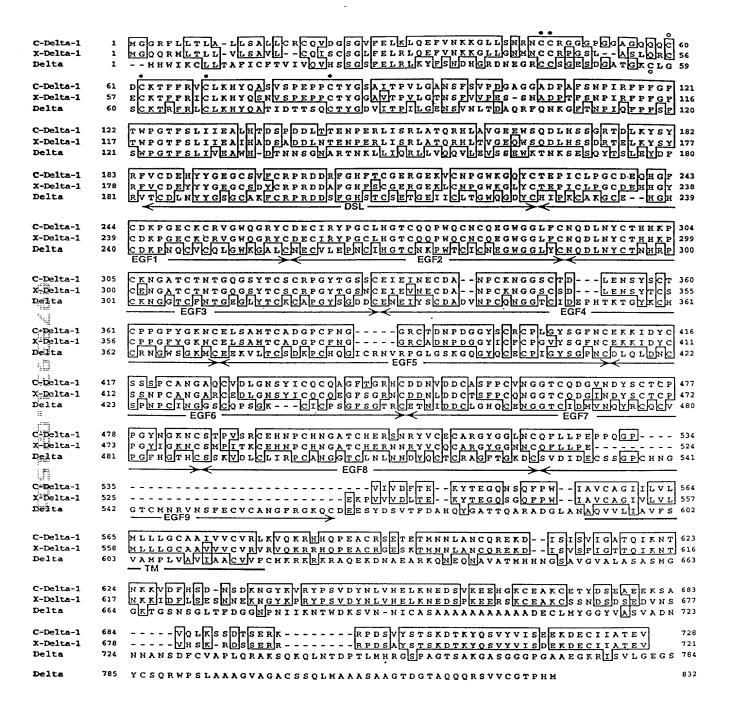
2830 TCTGCTTGTGTTTTCTCTCAACAGGTGTAAAAAAAGCTGACGTGGGAAAGCTT 2883

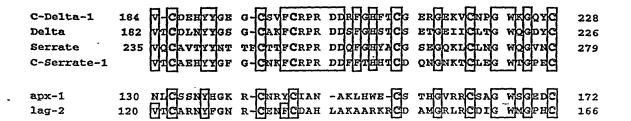


| 1 | MGGRFLLTLA | LLSALLCRCQ | VDGSGVFELK | LQEFVNKKGL | LSNRNCCRGG | GPGGAGQQQC | |
|-----|------------|-------------------|-------------------|-------------------|------------|----------------|--|
| 61 | DCKTFFRVCL | KHYQASVSPE | PPCTYGSAIT | PVLGANSFSV | PDGAGGADPA | FSNPIRFPFG | |
| 121 | FTWPGTFSLI | IEALHTDSPD | DLTTENPERL | ISRLATORHL | AVGEEWSQDL | HSSGRTDLKY | |
| 181 | SYRFVCDEHY | YGEGCSVFCR | PRDDRFGHFT | CGERGEKVCN | PGWKGQYCTE | PICLPGCDEQ | |
| 241 | HGFCDKPGEC | KCRVGWQGRY | CDECIRYPGC | LHGTCQQPWQ | CNCQEGWGGL | FCNODLNYCT | |
| 301 | HHKPCKNGAT | CINIGQGSYT | CSCRPGYTGS | SCEIEINECD | ANPCKNGGSC | TDLENSYSCT | |
| 361 | CPPGFYGKNC | ELSAMTCADG | PCFNGGRCTD | NPDGGYSCRC | PLGYSGFNCE | KKIDYCSSSP | |
| 421 | CANGAQCVDL | GNSYICQCQA | GFTGRHCDDN | VDDCASFPCV | NGGTCQDGVN | DYSCTCPPGY | |
| 481 | NGKNCSTPVS | RCEHNPCHNG | ATCHERSNRY | VCECARGYGG | LNCOFLLPEP | POGPVIVDFT | |
| 541 | EKYTEGQNSQ | FPWIAVCAGI | ILVLMLLLGC | AAIVVCVRLK | VOKRHHOPEA | CRSETETMNN | |
| 601 | LANCQREKDI | SISVIGATQI | KNTNKKVDFH | SDNSDKNGYK | VRYPSVDYNL | VHELKNEDSV ' | |
| 661 | KEEHGKCEAK | CETYDSEAEE | KSAVOLKSSD | TSERKRPDSV | YSTSKDTKYO | SVYVISEEKD | |
| | ECTTATEV | | - | | | · - | |









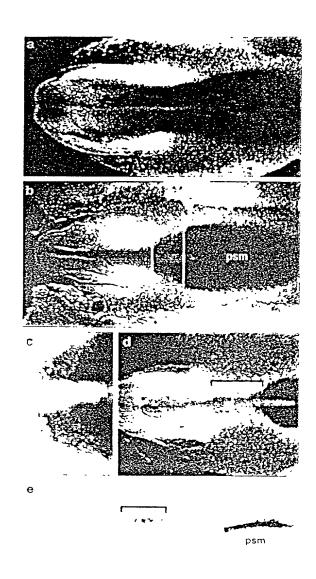


FIG. 5

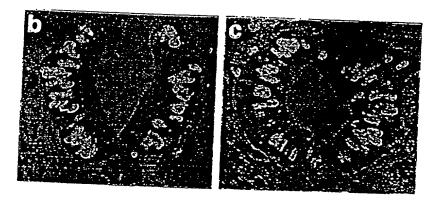


FIG. 6B

FIG. 6C

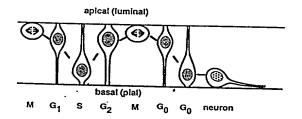
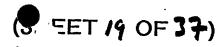


FIG. 6A



| CTGCAGGAAT | TCSMYCGCAT | GCTCCCGGCC | GCCATGGGCC | GTCGGAGCGC | GCTAGCCCTT | 60 |
|------------|------------|------------|------------|------------|------------|------|
| GCCGTGGTCT | CTGCCCTGCT | GTGCCAGGTC | TGGAGCTCCG | GCGTATTTGA | GCTGAAGCTG | 120 |
| CAGGAGTTCG | TCAACAAGAA | GGGGCTGCTG | GGGAACCGCA | ACTGCTGCCG | CGGGGGCTCT | 180 |
| GGCCCGCCTT | GCGCCTGCAG | GACCTTCTTT | CGCGTATGCC | TCAAGCACTA | CCAGGCCAGC | 240 |
| GTGTCACCGG | AGCCACCCTG | CACCTACGGC | AGTGCCGTCA | CGCCAGTGCT | GGGTGTCGAC | 300 |
| TCCTTCAGCC | TGCCTGATGG | CGCAGGCATC | GACCCCGCCT | TCAGCAACCC | CATCCGATTC | 360 |
| CCCTTCGGCT | TCACCTGGCC | AGGTACCTTC | TCTCTGATCA | TTGAAGCCCT | CCATACAGAC | 420 |
| TCTCCCGATG | ACCTCGCAAC | AGAAAACCCA | GAAAGACTCA | TCAGCCGCCT | GACCACACAG | 480 |
| AGGCACCTCA | ĆTGTGGGAGA | AGAATGGTCT | CAGGACCTTC | ACAGTAGCGG | CCGCACAGAC | 540 |
| CTCCGGTACT | CTTACCGGTT | TGTGTGTGAC | GAGCACTACT | ACGGAGAAGG | TTGCTCTGTG | 600 |
| TTCTGCCGAC | CTCGGGATGA | CGCCTTTGGC | CACTTCACCT | GCGGGGACAG | AGGGGAGAAG | 660 |
| ATGTGCGACC | CTGGCTGGAA | AGGCCAGTAC | TGCACTGACC | CAATCTGTCT | GCCAGGGTGT | 720 |
| GATGACCAAC | ATGGATACTG | TGACAAACCA | GGGGAGTGCA | AGTGCAGAGT | TGGCTGGCAG | 780 |
| GGCCGCTACT | GCGATGAGTG | CATCCGATAC | CCAGGTTGTC | TCCATGGCAC | CTGCCAGCAA | 840 |
| CCCTGGCAGT | GTAACTGCCA | GGAAGGCTGG | GGGGGCCTTT | TCTGCAACCA | AGACCTGAAC | 900 |
| TACTGTACTC | ACCATAAGCC | GTGCAGGAAT | GGAGCCACCT | GCACCAACAC | GGGCCAGGGG | 960 |
| AGCTACACAT | GTTCCTGCCG | ACCTGGGTAT | ACAGGTGCCA | ACTGTGAGCT | GGAAGTAGAT | 1020 |
| GAGTGTGCTC | CTAGCCCCTG | CAAGAACGGA | GCGAGCTGCA | CGGACCTTGA | GGACAGCTTC | 1080 |
| TCTTGCACCT | GCCCTCCCGG | CTTCTATGGC | AAGGTCTGTG | AGCTGAGCGC | CATGACCTGT | 1140 |
| GCAGATGGCC | CTTGCTTCAA | TGGAGGACGA | TGTTCAGATA | ACCCTGACGG | AGGCTACACC | 1200 |
| TGCCATTGCC | CCTTGGGCTT | CTCTGGCTTC | AACTGTGAGA | AGAAGATGGA | TCTCTGCGGC | 1260 |
| | GTTCTAACGG | | | | | 1320 |
| TGCCAGGCTG | GCTTCTCCGG | GAGGTACTGC | GAGGACAATG | TGGATGACTG | TGCCTCCTCC | 1380 |
| CCGTGTGCAA | ATGGGGGCAC | CTGCCGGGAC | AGTGTGAACG | ACTTCTCCTG | TACCTGCCCA | 1440 |
| CCTGGCTACA | CGGGCAAGAA | CTGCAGCGCC | CCTGTCAGCA | GGTGTGAGCA | TGCACCCTGC | 1500 |
| CATAATGGGG | CCACCTGCCA | CCAGAGGGGC | CAGCGCTACA | TGTGTGAGTG | CGCCCAGGGC | 1560 |
| TATGGCGGCC | CCAACTGCCA | GTTTCTGCTC | CCTGAGCCAC | CACCAGGGCC | CATGGTGGTG | 1620 |
| GACCTCAGTG | AGAGGCATAT | GGAGAGCCAG | GGCGGGCCCT | TCCCCTGGGT | GGCCGTGTGT | 1680 |
| GCCGGGGTGG | TGCTTGTCCT | CCTGCTGCTG | CTGGGCTGTG | CTGCTGTGGT | GGTCTGCGTC | 1740 |
| CGGCTGAAGC | TACAGAAACA | CCAGCCTCCA | CCTGAACCCT | GTGGGGGAGA | GACAGAAACC | 1800 |
| ATGAACAACC | TAGCCAATTG | CCAGCGCGAG | AAGGACGTTT | CTGTTAGCAT | CATTGGGGCT | 1860 |
| ACCCAGATCA | AGAACACCAA | CAAGAAGGCG | GACTTTCACG | GGGACCATGG | AGCCGAGAAG | 1920 |
| AGCAGCTTTA | AGGTCCGATA | CCCCACTGTG | GACTATAACC | TCGTTCGAGA | CCTCAAGGGA | 1980 |
| GATGAAGCCA | CGGTCAGGGA | TACACACAGC | AAACGTGACA | CCAAGTGCCA | GTCACAGAGC | 2040 |
| TCTGCAGGAG | | | | | | 2100 |
| AGGCCAGAGT | | | | | | 2160 |
| TCTGCAGAAA | | | | | | 2220 |
| AAATTCCCAT | | | | | | 2280 |
| GAGGAAGGGA | | | | | | 2340 |
| CTCTCAGAGT | | | | | | 2400 |
| GCCTGCTGGT | | | | | | 2460 |
| GACGAGTGAC | | | | | | 2520 |
| ATGAGCCAGT | | | | | | 2580 |
| | TTTTTTTTC | | | | | 2640 |
| TTTGTAAAAA | TATTTTTCAT | GATTATGGGA | GAGCTCCCAA | CGCGTTGGAG | GT | 2692 |
| | | | | | | |

FIG. 7



| 50 | NRNCCRGGSG | EFVNKKGLLG | SSGVFELKLQ | VVSALLCQVW | MGRRSALALA |
|-------|--------------------|------------|------------|------------|------------|
| 100 | FSLPDGAGID | AVTPVLGVDS | SPEPPCTYGS | VCLKHYQASV | PPCACRTFFR |
| 150 | ${\tt RLISRLTTQR}$ | PDDLATENPE | LIIEALHTDS | FGFTWPGTFS | PAFSNPIRFP |
| 200 | CRPRDDAFGH | HYYGEGCSVF | RYSYRFVCDE | DLHSSGRTDL | HLTVGEEWSQ |
| · 250 | ECKCRVGWQG | DQHGYCDKPG | TDPICLPGCD | CDPGWKGQYC | FTCGDRGEKM |
| 300 | CTHHKPCRNG | GLFCNQDLNY | WQCNCQEGWG | GCLHGTCQQP | RYCDECIRYP |
| 350 | SCTDLEDSFS | CAPSPCKNGA | GANCELEVDE | YTCSCRPGYT | ATCTNTGQGS |
| 400 | HCPLGFSGFN | SDNPDGGYTC | DGPCFNGGRC | VCELSAMTCA | CTCPPGFYGK |
| 450 | DNVDDCASSP | QAGFSGRYCE | DLGNSYLCRC | SPCSNGAKCV | CEKKMDLCGS |
| 500 | NGATCHQRGQ | VSRCEHAPCH | GYTGKNCSAP | VNDFSCTCPP | CANGGTCRDS |
| 550 | GPFPWVAVCA | LSERHMESQG | EPPPGPMVVD | GGPNCQFLLP | RYMCECAQGY |
| 600 | NNLANCQREK | EPCGGETETM | LKLQKHQPPP | GCAAVVVCVR | GVVLVLLLLL |
| - 650 | YNLVRDLKGD | SFKVRYPTVD | FHGDHGAEKS | QIKNTNKKAD | DVSVSIIGAT |
| 700 | PESVYSTSKD | RGGEIPDRKR | AGEEKIAPTL | RDTKCQSQSS | EATVRDTHSK |
| 722 | | | EV | AEKDECVIAT | TKYQSVYVLS |

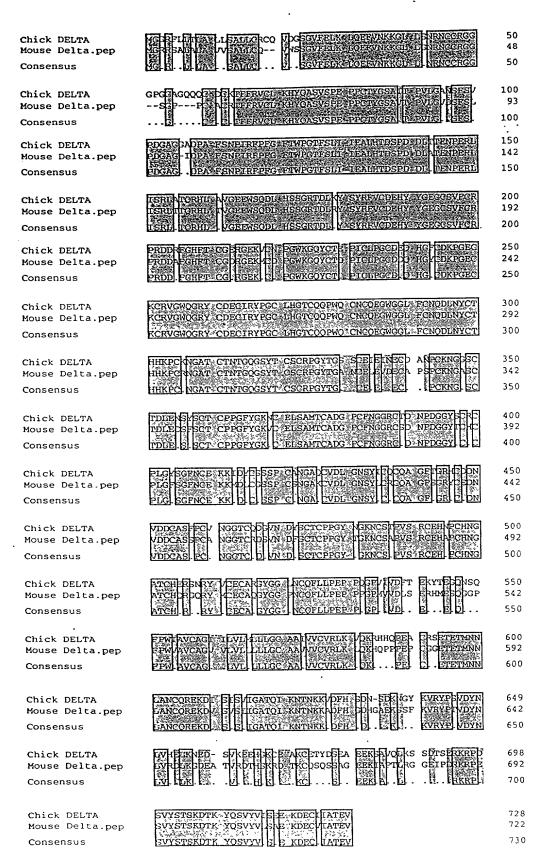


FIG. 9

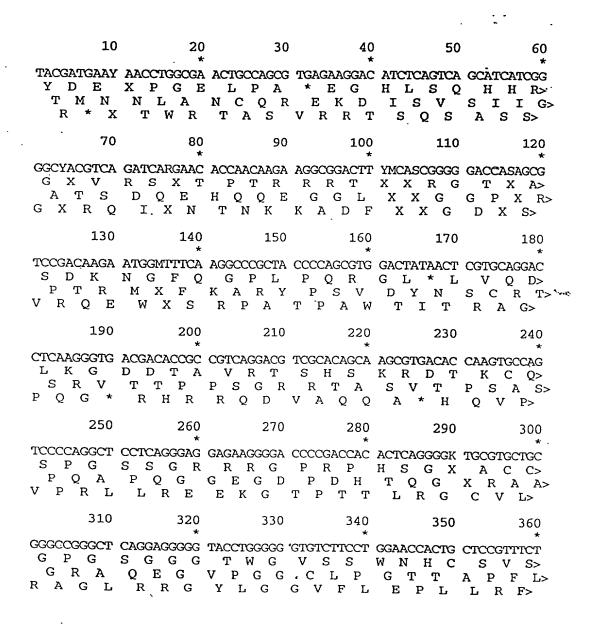


FIG. 10

370 380 390 400 410 420 CTTCCCAAAT GTTCTCATGC ATTCATTGTG GATTTTCTCT ATTTTCCTTT TAGTGGAGAA L P K C S H A F I V D F L Y F P F S G E>
F P N V L M H S L W I F S I F L L V E K>
S S Q M F S C I H C G F S L F S F * W R> 430 440 450 460 470 480 GCATCTGAAA GAAAAAGCC GGACTCGGGC TGTTCAACTT CAAAAGACAC CAAGTACCAG A S E R K R P D S G C S T S K D T K Y Q>
H L K E K G R T R A V Q L Q K T P S T S>
S I * K K K A G L G L F N F K R H Q V P> 500 520 TCGGTGTACG TCATATCCGA GGAGAAGGAC GAGTGCGTCA TCGCA S V Y V I S E E K D E C V I A> R C T S Y P R R R T S A S V G V R H I R G E G R V R H

FIG. 10 (cont'd)

| Ţ | TMNNLANCQREKDISVSIIGATQIXNTNKKADFXXGDXSSDKNGFQKARY | 50 |
|------|--|-----|
| | 711111111111111111111111111111111111111 | |
| 597 | TMNNLANCQREKDISISVIGATQIKNTNKKVDFHSDNSDKNGY.KVRY | 643 |
| 51 | PSYLDANI MODI MODIAN MARKAMBANA SAGARARA SAGARA SAGARA SAGARA SAGARARA SAGARA SAGARARA SAGARA SAGAR | |
| 21 | PSVDYNLVQDLKGDDTAVRTSHSKRDTKCQSPGSSGRRRGPRPHSGXACC | 100 |
| 644 | PSVDYNLVHELKNED.SVKEEHGKCEAKCETYDSEAEEKSA | 602 |
| | · · · · · · · · · · · · · · · · · · · | 003 |
| 101 | GPGSGGGTWGVSSWNHCSVSLPKCSHAFIVDFLYFPFSGEASERKRPDSG | 150 |
| co.4 | :: ::. . | |
| 684 | VQLKSSDTSERKRPDSV | 700 |
| 151 | CSTSKDTKYQSVYVISEEKDECVIA 175 | |
| 101 | : | |
| 701 | YSTSKDTKYQSVYVISEEKDECIIA 725 | |
| | | |

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| 10 * * | 20 * * | * * | 40 * * | 50 * * | 60 * * |
|-------------|--------------|------------|------------|----------------|------------|
| CATTGGGTAC | GGGCCCCCCT | CGAGGTCGAC | GGTATCGATA | AGCTTGATAT | CGAATTCCGG |
| 70 * * | 80 * * | 90 * * | 100 * * | 110 * * | 120 * * |
| | CCGGGCACCT | TCTCTCTGAT | TATTGAAGCT | CTCCACACAG | ATTCTCCTGA |
| 130 * * | 140 * * | 150 * * | 160 * * | 170 * * | 180 |
| 'IGACCTCGCA | ACAGAAAACC | CAGAAAGACT | CATCAGCCGC | CTGGCCACCC | AGAGGCACCT |
| 190 * * | 200 | 210 | 220 | 230 | 240 * * |
| | CAGGAGTGGT | CCCAGGACCT | GCACAGCAGC | GGCCGCACGG | ACCTCAAGTA |
| 250 * * | × × | 270 | 280 * * | 290 * * | 300 * * |
| | | | | | TTTTCTCCCG |
| 310 | 320 | 330 | 340 | 350 | 360 * * |
| | | | | CGTGGGGAGA | |
| 370 | 380 * * | 390 * * | 400 * * | 410 | 420 * * |
| CCCTGGCTCG | | | | CTGCCTGGAT | |
| 430 | 440 | 450 | 460 | 470 * * | 480 |
| | | | | GIGGGCTGGC | |
| 490 * * | 500 | 510 | 520 | 530 * * | 540 |
| | 'L'GTATCCGCT | ATCCAGGCTG | TCTCCATGGC | ACCTGCCAGC | AGCCCTGGCA |
| 550 * * | 560 | 570 | 580 | 590 | 600 * * |
| | | | | CAGGACCTGA | |
| 610 | 620 | 630 | 640 | 650 * * | 660 |
| ACACCATAAG | CCCTGCAAGA | ATGGAGCCAC | CTGCAACAAA | CACGGGCCAG | GGGGAGCTAC |
| 670 | 680 | 690 | 700 | 710 * * | 720 |
| ACTTGGTCTT | 'IGGCCGGNCT | GGGGTACANA | GGGTGCCACC | TGCGAAGCTT | GGGGATTGGA |
| 730 | 740 | 750 * * | 760 | 770 | 780 |
| CGAGTTGTTG | | | | 'l'IGACGGA'I'C | TTCGGAGAAC |
| 790 * * | * 800 | 810 | 820 * * | 830 * * | 840 |
| AGCTACTCCT | | | | TCIGIGVYTI. | |
| 850 * * | | 870 | 880 | 890 | |
| | | | | CAGACAGCCC | |

FIG. 12A

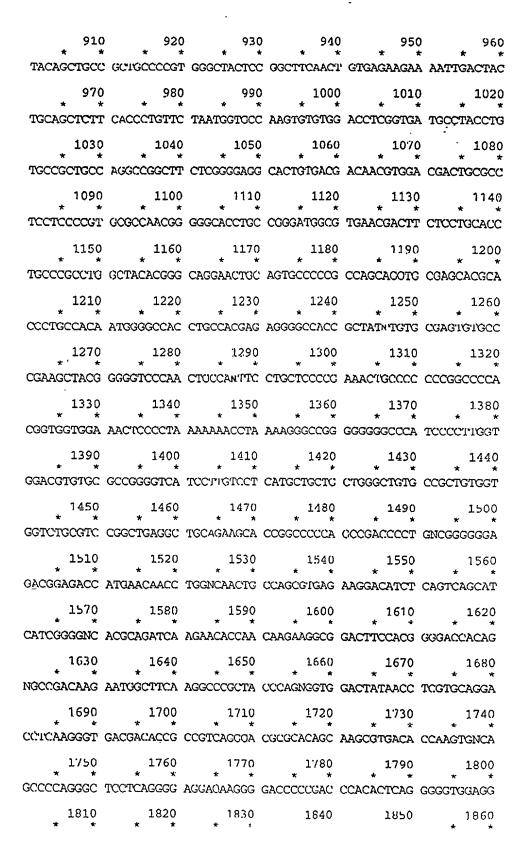


FIG. 12A (cont'd)

AAGCATCITG AAAGAAAAAG GCCGGACTTC GGGCTTGITC AACTITCAAA AGACAANCAA

1870 1880 1890 1900 1910 1920

NGTACAAGTC GGTGINCGTC ATTICCGNAG GAGGAAGGNT GACIGCGTCA TAGGAANTTG

1930 1940 1950 1960 1970 1980

AGGTNGIAAA NICGNAGTTG ANNIIGCAAA GNNVICCCCG GATTCCGNIT TCAAAGTTTT



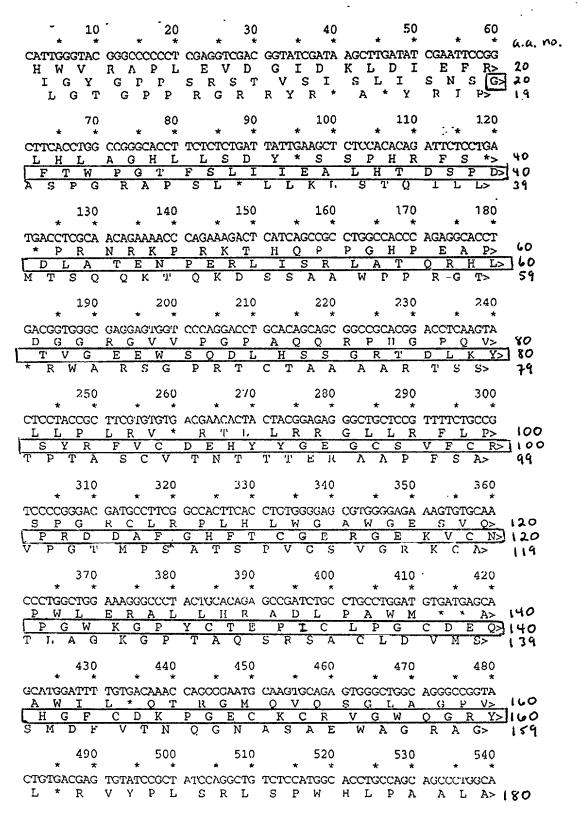


FIG. 12B

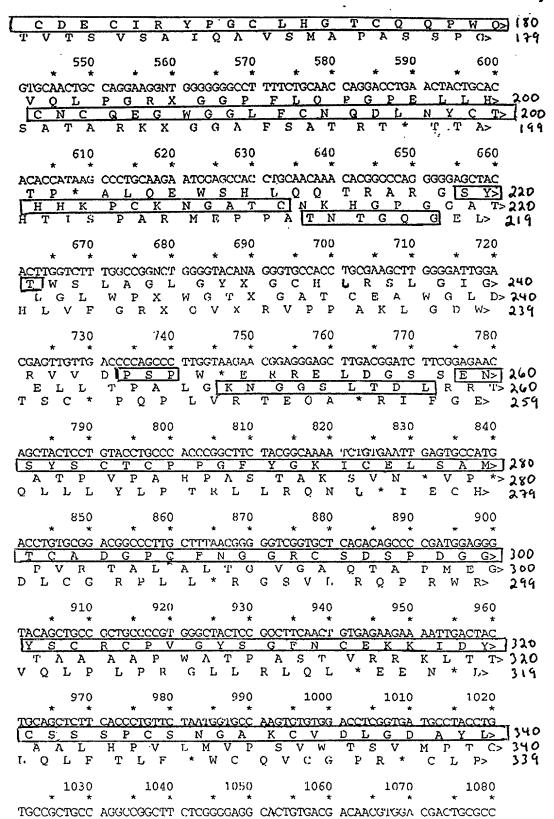


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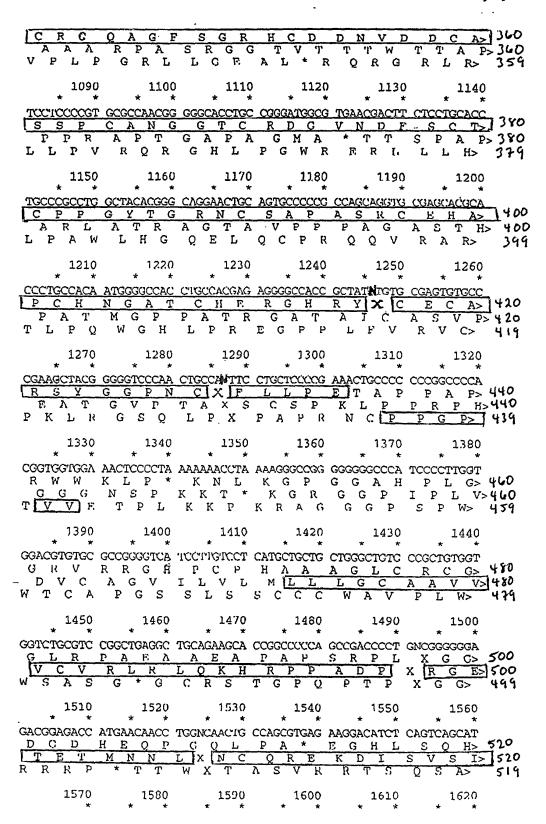


FIG. 12B (cont'd)

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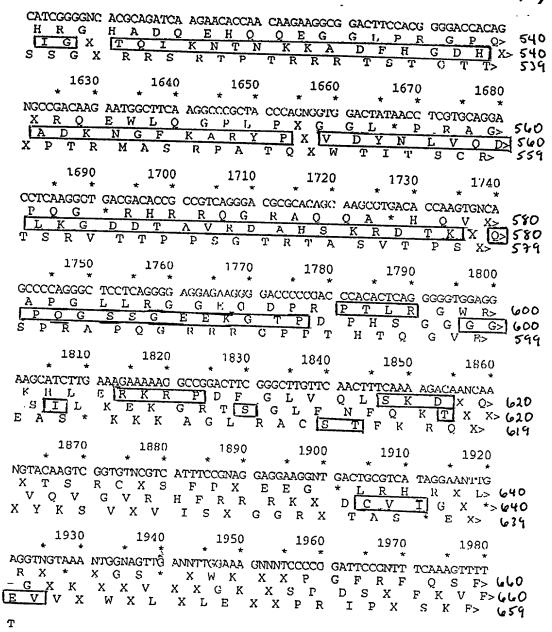
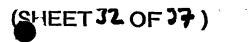
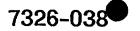
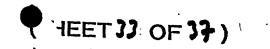


FIG. 12B (cont'd)



| Consensus GTCCAGCGGT ACCATGGGCC GTCGGAGCGC GCTAGCCCTT CCCGTG | |
|--|-----------------------|
| andmicross Demishaba assaulado parugual Affasi | GGTCT 50 |
| Mouse Delta DNA CTGCCCTGCT GTGCCAGGTC TGGACCTCCG GCGTATTTGA GCTGAY | |
| Consensus CTGCCCTGCT GTGCCAGGTC TGGAGCTCCG GCGTATTTGA GCTGAA | AGCTO 100 |
| Mouse Delta DNA CAGGAGTTCG TCAACAAGAA GGGGCTGCTG GGGAACCGCA ACTGCT | recce 150 |
| Consensus Caggagites Tearchagan eggectete eggareega actes | rgccg -150 |
| Mouse Delta DNA CGGGGGCTCT GGCCCGCCTT GCGCCTGCAG GACCTTCTTT CGCGTA Human Delta | ATGCC 200 |
| Consensus CGGGGGCTCT GGGCCGCCTT GCGCCTGCAG GACCTTCTTT CGGGTA | ATGC C 200 |
| Mouse Delta DNA TCAACCACTA CCAGGCCAGC GTGTCACCGG AGCCACCCTG CACCTA | |
| Consensus TCAAGCACTA CCAGGCCACC GTGTCACCGG AGCCACCCTG CACCTA | ACGGC 250 |
| Mouse Delta DNA AGTGCTGTCA CGCCAGTGCT GGGTGTCGAC TCCTTCAGCC TGCCTG | |
| AGTGCTGTCA CGCCAGTGCT CCGTGTCGAC TCCTTCAGCC TGCCTS | |
| Mouse Delta INVA definition by Contraction | |
| Consensus dehladderde byleddadd helydddidd benylabegyyy barthre | |
| Mouse Delta DNA INCGGCTTCA CCTGGCCGG INCCTTCTCT CTGATLATTG AAGCTC Human Delta INCGGCTTCA CCTGGCCGG INCCTTCTCT CTGATLATTG AAGCTC | TCCA 105 |
| Consensus The Court of the Consensus The Consensus Consensus The Consens | |
| Mouse Delta DNA TACAGATTCT CC GATGACC TCGCAACAGA AAACCCAGAA AGACTC CACAGATTCT CC GATGACC TCGCAACAGA AAACCCAGAA AGACTC CACAGATTCT CC GATGACC TCGCAACAGA AAACCCAGAA AGACTC | ATCA 155 |
| | |
| Mouse Delta DNA GCCGCCTGC CACCAGAGG CACCTGACAG TGGGGAGA TTGGTC Human Delta GCCGCCTGC CACCAGAGG CACCTGACAG TGGGGAGA TTGGTC CODSERSUS GCCGCCTGC CACCAGAGG CACCTGACAG TGGGGAAGA TTGGTC | CAG 205 |
| | |
| Mouse Delta DNA GACCTICACA GHAGCGGCCG CACGACCTC CGTACTCHT ACCGCT Human Delta GACCTICACA GHAGCGGCCG CACGACCTC AGTACTCHT ACCGCT Consensus GACCTICACA GHAGCGGCCG CACGACCTC HETACTCHT ACCGCT | |
| | |
| Mouse Delta DNA STGTGACGAS CACTACTACG GAGA-GGITG CTC/GTUTTC TGCCGA Human Delta GTGTGACGAA CACTACTACG GAGA-GGITG CTC/GTUTTC TGCCGA Consensus GTGTGACGAR CACTACTACG GAGA-GGITG CTC/GTUTTC TGCCGA | |
| Mouse Delea DNA GGGATGA GC CTTTGGCCAC TTCACCTGTG GGGATAGGG GGAGAA Human Delea GGGATGATGC CTTTGGCCAC TTCACCTGTG GGGATGAGG GGAGAA Consensus GGGATGATGC CTTTGGCCAC TTCACCTGTG GGGATGAGG GGAGAA | ACTC 355 |





| House Delta Human Delta Consensus | DNA | TECHACCOTE GOTEGAAAGO CONTRACTEC ACHGALCOAA TOTELOTECO TECHACOOTE GOTEGAAAGG CONTRACTEC ACHGALCOTA TOTELOTECO TECHACOOTE GOTEGAAAGG CONTRACTEC ACHGALCOTA TOTELOTECO | 693 405 700 |
|---|-------|--|----------------------|
| Mouse Delta Human Delta Consensus | | ACCUTETEAT CALCANCATE GATACTETEA CARACCAGGE GATTECAAGT TECHTOTEAT CALCANCATE GATTHTOTEA CARACCAGGE GATTECAAGT . WCCTTETEAT CALCATE GATWATETEA CARACCAGGE GATTECAAGT | 743 455 750 |
| Mouse Delta Human Delta Consensus | DNA | SCAGAGTIGG CTGGCAGGGC CGTTACTG C ANGAGTGTAT CCGATALCCA GCAGAGTGG CTGGCAGGGC CGTTACTGHG AGGAGTGHAT CCGATALCCA GCAGAGTGGG CTGGCAGGGC CGGTACTGHG ANGAGTGHAT CCGATALCCA | 793 505 800 |
| Mouse Delta Human Delta Consensus | DNA · | GETTGTCTCC ATGGCACCTG CCAGCANCCC TGGCAGTGTA ACTGCCAGGA GG TGTCTCC ATGGCACCTG CCAGCANCCC TGGCAGTGTA ACTGCCAGGA GGTTGTCTCC ATGGCACCTG CCAGCANCCC TGGCAGTGNA ACTGCCAGGA | 843 555 850 |
| Mouse Delta Human Delta Consensus | אמט | AGG TEGGEG GECCTTTTCT GCAACCAPGA CCTGAACTAC TETACTCACC AGG TEGGEG GECCTTTTCT GCAACCACGA CCTGAACTAC TECACCACC AGG TEGGEG GECCTTTTCT GCAACCA GA CCTGAACTAC TECACCACC | 893 605 900 |
| Mouse Delta Human Delta Consensus | UNA | ATAAGCCTTG CALGAATGGA GCCACCTGCA CLAACACG GCCAGGGG A ATAAGCCTTG CAAGAATGGA GCCACCTGCA ACAACACGG GCCAGGGGA ATAAGCCTTG CALGAATGGA GCCACCTGCA ACAACACGG GCCAGGGG A | 941 655 950 |
| Mouse Delta Human Delta Consensus | DNA | GCTACACHTG HTCHT-CCC KIRCHGGGT ANALAGGTG CCAACTGTG-GCTACACHTG HTCHTTGCCC GRICHGGGT ALANAGGTG CCAACTGTGA | 986 705 1000 |
| Monee Delta Human Delta Consensus | DNA | ACCTITICATE ATTEMACE TO TO TO ACCOUNTSY ARCANCEAGE ACCTITICATE ATTEMACE TO TO THE ACCOUNTSY ARCANCEAGE ACCTITICATE ATTEMACE TO THE ACCOUNTSY ARCANCEAGE | 1031 755 1050 |
| Mouse Delta Human Delta Consensus | DNA | COACCTOCAC COALCTT-6 ACTACACT CTCUTCLACC TOCCOLCCCG COACCTTCAC COALCTTCCG ACAACACCTA CTCTTCTACC TOCCCACCCG COACCTKSAC COALCTTCCG ACTACACCTW CTCUTCHACC TOCCCACCCG | 1079 805 1100 |
| Mouse Delta Human Delta Consensus | ANG | GETTETATIGG CAARGTETET GASTIGACTE CEATGACTE TECHGALIGGE GETTETAGGE CAARATETET GARTIGAGIG CEATGACCTE TOCHGALGGE GETTETAMG CAARATETET GARTIGAGIG CEATGACCTE TOCHGALGGE | 1129 055 1150 |
| Mouse Delta Human Delta Consensus | DNA | CCTTGCTTIA ANGGREGACO ATOMICAGAN ASCCOMANG GAGGITACAS CCTTGCTTIA ACGGREGACO HIGHICAGAN ASCCOMANG GAGGITACAS CCTTGCTTIA ANGGREGACO HIGHICAGAN ANCCOMANG GAGGITACAS | 1179 905 1200 |
| Mouse Delta Human Delta Consensus | DNA | CTGCCATTGC CCCTTGGGCT ICTCTGGCTT CAACTGTGAG AAGAALATTG CTGCCGCTGC CCCTTGGGCT ICTCGGGCTT CAACTGTGAG AAGAALATTG CTGCCRYTGC CCCTTGGGCT ICTCGGCTT CAACTGTGAG AAGAALATAG | 1229 955 1250 |
| Mouse Delta Human Dolta Consensus | DNA | ATCTCTGGGG CTCTTGCCT TGTTCTAATG GTGCCAAGTG TGTGGACCTC ACTACTGGG CTCTTCACCT TGTTCTAATG GTGCCAAGTG TGTGGACCTC MYVWCTGGGG CTCTTGCCCY TGTTCTAAAG GTGCCAAGTG TGTGGACCTC | 1279 1005 1300 |

FIG. 13 (cont'd)

| Mouse Delta DNA Kuman Delta Consensus | GCYALTCHT ACCTGTGCCG TTGCCAGGCT GGCTTCTCTG GGAGGTACTG | 1325 1055 1350 |
|---|--|----------------------|
| Mouse Delta DNA Ruman Delta Consensus | ACT CYCYN, REGOVENCE. CHECCECCE CCCELCHECH WYRCCECCY ACT CYCYN: CHECYCOYC. CHECCECCEC CCCELCHECH WYRCCECCY ACT CYCYN. CHECYCOYC. CHECCECCEC CCCELCHECH WYRCCECCY ACT CYCYN. CHECYCOT. CHECCECCEC CCCELCHECH WYRCCECCY AND COCH CHECK COCH CAN | - 1379 1109 |
| Mouse Delta DNA Human Delta Consensus | CCTGCCGGGA CAGTGTGAAC GACTTCTCCT GTACCTCCCC CCTGGCTACCCTGCCGGGA TGGTGTGAAC GACTTCTCCT GTACCTGCCC CCCTGGCTACCCCTGCCGGGA XAGAGTGAAC CACTTCTCCT GAACCTGCCC ACCTGGCTAC | 1429 1155 1450 |
| Mouse Delta DNA Human Delta Consensus | ACGGGCANGA ACTGCAGTGC CCCCONCAGC AGGTGTGAGC ATGCACCCTG ACGGGCANGA ACTGCAGNGC CCCCONCAGC AGGTGTGAGC ANGCACCCTG ACGGGCANGA ACTGCAGNGC CCCNGNCAGC AGGTGTGAGC ANGCACCCTG | 1479 1205 1500 |
| Mouse Delta DNA Auman Delta Consensus | CCATAATGGG GCCACCTGCC ACTAGAGGGG CCACGCTAC ATGTGTGAGT CCACAAATGGG GCCACCTGCC ACTAGAGGGG CCACGGTAT TITGTGGAGT CCAMAATGGG GCCACCTGCC ACTAGAGGGG CCACGGTAY WIGTGMGAGT | 1529 1255 1550 |
| Monse Delta DNA Human Delta Consensus | GOGCCONGG CTANGGOGG CCCAACTGCC APTRICTGCT CCCGAAACTGGGGGGGGGGGGGGGGGGGGGGGGG | 1578 1305 1600 |
| House Delta DNA Human Delta Consensus | -XCONCONGG FCCCANGGTG GTGG-ANCTC ACTOMARAR ACTIMARACE GCCCCCCGG FCCCANGGTG GTGGNANCTC HSYNAMARRM AMMTARRACE | 1625 1355 1650 |
| Mouse Dolta DNA Muman Delta Consensus | GCC GGG GCCC TCCCCC TCCTCCCC TGTGGCGG GGTGGTGTT GCCGGGGGG GCCCTCCCC TCCCTCCTCG TGTGGCGG GGTCATCCTT GCCGGGGGG GCCCTCCCCC TCCCCCC TGTGGCGG GGTCATCCTT | 1675 1405 1700 |
| Mouse Delta DNA Human Delta Consensus | GTCCTC TGC TGCTGCTGGG CTGTGCTGGT GTGGTGGTCT GCGTCCGGCT GTCCTC TGC TGCTGCTGGG CTGTGCCGCT GTGGTGGTCT GCGTCCGGCT GTCCTCMTGC TGCTGCTGGG CTGTGCTGGT GTGGTGGTCT GCGTCCGGCT | 1725 1455 1750 |
| Mouse Delta DNA Human Delta Consensus | GANGETYCAG AANGACONGO OTGCANGTIGA NGCCTGTGGG GGYGAGACNG GALGCTGCAG AALGACONGO OTGCANGTGA CCCTGNGGG GGYGAGACNG GANGCTGCAG AANGACONGO ONGCANGNA NGCCTGNGGG GGYGAGACNG | 1775 1505 1800 |
| Mouse Della DNA Human Delta Consensus | MACCATGAA CAACCTACK AATTGCCAGC GTGAGAAGGA CATHTCTGTT | 1825 1555 1850 |
| Mouse Delta DNA Human Delta Consensus | AGCATCATIG GGG-TACTCA GATCAAGAAC ACCAACAAGA AGGCGGACTT AGCATCATTG GGGVCACTCA GATCAAGAAC ACCAACAAGA AGGCGGACTT AGCATCATTAG GGGVACTCA CATCAAGAAC ACCAACAAGA AGGCGGACTT | 1875 1605 1900 |
| Mouse Delta DNA Human Delta Consensus | TCACGCGAC CAPGGGCA ADAAGADCAG CTTHAAGGIC CGATACCCDA CCACGCGCAC CACAGAGGCCB ACAAGADTGG CTTLAAGGIC CGTTACCCDG ACACGCGGGAC CAPTACCCDG ACACGCGAGACTGG CTTMAAGGIC CGMTACCCMR | 1925 1655 1950 |

FIG. 13 (cont'd)

| - | Modse Della vs Famal Human Della |
|---|--|
| Mouse Delta DNA Human Delta Consensus | CTGTGGACTA TAACCTCGTP CLAGACCTCA AGGGAGATGA AGCCACGTC 1975 NGGTGGACTA TAACCTCGTS CAGGACCTCA AGGGAGATGA CACCACGTC 1705 |
| | NINGTOGACTA TAACCTCCTK CRESACCTCA AGGGGGANGA TECCECCETC 2000 |
| Mouse Delta DNA Human Delta | AGGGATACAC ACAGCAARCG TGACACCAAG TGCAGTGAC AGAGCTGTGC 2025 |
| Consensus | AGGGANTON ACAGCAANCE TOACACCAAG TOXCAGCOC AGGGCTCTCC 2025 AGGGANTON ACAGCAANCE TOACACCAAG TOXCAGCOC AGGGCTCTCC 2050 |
| Mouse Delta DNA Human Delta | AGGAGAGAG ANGANGE COCOMACA COUNT PROCESS COLORS |
| Consensus | ACCORDAGGA ANGGODALCE CCTACCTACA CTTATGGGGT GGAGGAAGA 1805 ACCORDAGGA ANGGGGALCE CCTACCTACA CTTATGGGGT GGAGGAAGAW 2100 |
| Mouse Delta DNA Ruman Delta | TICHTGALAGA AAAAGGCCOG ALTILT-GIC TRATTOHAGET TOOLS |
| Consensus | TCHTGANAGA AAAAGGCCEG ANTYGGGYY TRYTCHACHT TCAAAAGACA 1855 |
| Mouse velta DNA Human Delta | -ACTANGTAC PAGTOGOTOT NIGHTOTIVIC HOTAGNAL IN ACCESSIVE |
| Consensus | ANCHANGTAC MAGTCGGTGT MCTMTHTC CHAGTAGGA AGGMTGATTG 1905 ANCHANGTAC MAGTCGGTGT MCTMTHTC MCNAGTAGGA AGGMTGATTG 2200 |
| Mouse Delta DNA Human Delta | TOTIATA CE GACTGAGCT GTAABATGGA AGEGATSTGB CAAAATTECC 2208 COTTATACGA ANTIGAGGTN GTAAANTGGN AGTTGANTIT 1945 |
| Consensus | VGTMATA GM RNYTGAGGTN GTAARNIGGN AG-GATOTGS CAANNITECC 2250 |
| Mouse Delta DNA Human Delta | ATTTCTCTOA AATTAAAATTC CAACCATTA |
| Consensus | ATTICTCKSA AAKNNNATIC CMCGATATA GOYCOOTT |
| Mouse Deita DNA Human Deita | GAGACGAAGG GAGACGAAAT CCAUGGACTG LITUTTAGAA CCACCACACACACACACACACACACACACACACAC |
| Consensus | GAGAGGAAAC CCAGGGACTG MIKYTTAGAA CGAGGGACTG |
| Mouse Delta DNA Human Dolta | GCGAAGCTGG TTCTCTCAGA GTTAGCAGAG GCGCCCGACA CTCCCCCACA |
| Consensus | GCGAAGCTGG TTCTCTCAGA GTTAGCAGAG GCGCCCGACA CTCCCACA |
| Mouse Delta DNA Human Delta | AGGCTTTGGC TGCCCCTGGA CTGCCTGCTG GITGTTCCCA TTGCCCTC |
| Consensus | AGGCTTTGGC TGCCGCTGGA CTGCCTGCTG GTTGTTCCCA TTGCACTATG 2450 |
| Mouse Delta DNA Human Delta | GACAGITECT TOOLAGACTA TO |
| Consensus | GACAGTTGCT TTGAAGAGTA TATATTTAAA TGGACGAGTG ACTTGATTCA 2458 GACAGTTGCT TTGAAGAGTA TATATTTAAA TGGACGAGTG ACTTGATTCA 2500 |
| Mouse Delta DNA Human Delta | TATACGAAGC ACCURCTOUR CONTINUE |
| Сонвелѕиѕ | TATAGGAAGC ACGCACTGCC CACACGTCTA TCTTGGATTA CTATGAGCCA 2508 1981 2508 |
| Mouse Delta DNA | GTCTTTCCTT GARCTACAA |
| Consensus | GTCTTTCCTT GAACTACAAA CACAACTGCC TTTATTGTCC TTTTTGATAC 2558 |
| | GTCTTTCCTT GAACTAGAAA (ACAACTGCC TTTATTGTCC TTTTTGATAC 2600 |

FIG. 13 (cont'd)

| Kouse Delta Human Delta | DNA | | | | | CCTGTGTTAT | 2608 1981 |
|----------------------------|-----|------------|------------|-------------|------------|---------------------|--------------|
| Consensus | | TGAGATGTGT | TTTTTTTTT | CCTAGACGGG | AAAAAGAAAA | CGTGTGTTAT | 265 |
| Mouse Delta Human Delta | DNA | _ | | | GATATCTGTA | AAGCTTGAGT | 2656 1981 |
| Consensus | | TTTTTTGGGA | TTTGTAAAAA | TATTTTCAT | GATATCTGTA | AAGCTTGAGT | 2700 |
| Mouse Delta Human Delta | DNA | | | | Antiticcia | ANTATGTACA | 2708 1981 |
| Consensus | | ATTTTGTGAC | GTTCATTITT | ALLITARIVAL | antitegera | ANTATGTACA | 2750 |
| Mouse Delta Human Delta | DNA | | | | TTT1GTATAT | AAATGTATTT | 2758 1981 |
| Consensus | | AAGGCACTIC | GGGTCTATGT | GACTATATTT | тттгстатат | AAATGTATTT | 2800 |
| iouse Delta iuman Delta | UNA | | | | TTTTACTGTT | TTGTTAATGA | 2808 1981 |
| Consensus | | ATGGAATATT | GTGCAAATGT | TATTTGAGTT | TTTTACTGTT | TTGTT'AA TGA | 2850 |
| Mouse Delta Numan Delta | DNA | | | | ATAAATAAA | | 2857 1981 |
| onsensus | | AGAAATTCAT | ΤΤΤΑλΑλΛΤΑ | TITTTCCAAA | Αταλατατα | ግ ሬክልርጥልርል | 2899 |

G F T W P G T F S L I I E A L H T D S P DS DLA TEN PERL I SRLAT QRH L> 41 TVGEEWSQDLHSSGRIDLKY> 61 SYRFVCDEHYYGEGCSVFCR> 81 PRD DAFGH<u>FTCGERGEKVCN> [0]</u> PGWKGPYCTEPICLPGCDEQ> 121 HGFCDK PGEC KCR VGW OGR Y> 141 CDECIRYPGC LHGTCQ PWO> [6] CNCQEGWGGLFCNQDLNYCT> 181 T G Q G * 198 HHK PCK NGAT C * T N * KN GGS L T D L * 213 SYT # PSP ENSYS CTCPPGFYGKICELSAM 235 T.CADGPGFNGGRCSDSPDGG> 255 YSCRCPVGYSGFNCEKKIDY> 275 IJ CSSSPCSNGAKCVDLGDAYLD 295 a wille CRCQAGFSGRHCDDNVDDCA>'315 ië. SSPCANGGTCRDGVNDF-SCT> 335 - i CPPGYTGRNCSAPASRCEHA> 355 100 PCH NGAT CHERGH RY C E C A> 374 * RSYGGPNC * FLLPE * PPGP*391 * LL LGCAAVVVCVRLRLQKH>412 v v RPPADP * RGETETMNNL * 428 NC QRE KDI SVSI IG * T Q I K N T N > 449 KKA DFH GDH ADK.NGFKARYP * 469 V DYN LVOD LKG DDT AVRD AHSKRD TK* 495 OPOGSSGEEKGTP * PTLR * 66 * 514 Ī * RKRP * S * ত্ত কু * S K D * T * 526 CVT * E V * 531

FIG. 14